Curtis Lin, Ph.D. MIDS

curtiscjlin@outlook.com | https://linchunjen.github.io/ | San Francisco Bay Area

SUMMARY

A biologist/data scientist has experience in leading or supporting preclinical therapeutic antibody discovery and development, data-driven biomarker discovery and MOA studies, cell-based assay development, CRO/CDMO identification and management, cell manufacturing quality control and project management. Worked with crossfunctional teams on tech transfer to GMP environment, internal and external collaboration, and strategic planning.

Experienced in analysis and management of large volume multi-dimensional data and images using Python and R programming, machine learning algorithms, convolutional neural network, cloud computation, parallel computation with the MapReduce programming paradigm and Spark, SQL database, and data visualization. (Personal website: https://linchunjen.github.io/)

EXPERIENCE

AbVision Inc. – Associate Director, Research and Development, Milpitas, CA Senior Scientist, Research and Development, Milpitas, CA

Aug 2019 – present June 2018 – present

- Lead the program of early-phase discovery and preclinical development of therapeutic monoclonal antibodies and bispecific antibodies of Immuno-Oncology.
- Initiate and lead the development of novel platform of therapeutic antibody discovery with B cell sorting, single cell immune profiling with NGS, and unsupervised machine learning algorithms.
- Plan, design, and manage protein and antibody production and preclinical *in vivo* efficacy and toxicology studies with domestic and international CROs.
- Design and support early development of tumor-reactive T cells therapy and immune cell-based assays.
- Established academic and industry collaborations to support pipeline programs and outline development plans.
- Prioritize projects, allocate resources, coordinate team, and provide technical leadership to support timeline.
- Supervise and manage junior scientists and postdocs with resource and technical supports.

School of Information, UC Berkeley – Master student, Berkeley, CA

Aug 2018 - Aug 2020

- Developed an intelligent system that integrates electronic medical records, X-ray images, and deep learning insights to empower radiologists' diagnoses and workflows. (https://groups.ischool.berkeley.edu/chestx_ai/)
- Built a system on edge device to capture American Sign Language (ASL) and automatically convert ASL to audio with convolutional neural network.

SanBio Inc. – Scientist II, Quality Control, Mountain View, CA Scientist II, Research, Mountain View, CA

Jan 2018 - June 2018 June 2016 - Dec 2017

- Led and planed data-driven biomarker projects and executed biomarker development strategies to generate, analyze, and interpret data from clinical manufacturing studies.
- Developed, optimized, tech transferred and validated assays to GMP environment.
- Established data management and analysis pipeline of microarray and sequencing data.
- Worked with cross-functional teams to oversee and troubleshoot on-going product testing in CDMO and CTL.
- Reviewed documentation include standard procedures (SOP), deviations, tech transfer reports, batch records, qualification reports, validation reports, and specifications during cell product development.
- Developed biomarker-based qPCR assays to assist in-process control and supported process validation of cell manufacturing process and scale-up production for phase 2/3 clinical trials.
- Planed, executed, and documented analytical studies such as limits of detection, linearity, and reproducibility.

Department of Systems Biology, MD Anderson Cancer Center Postdoc Fellow; Houston, TX Aug 2011 – Oct 2015

- Executed and managed a 3.5 million DoD-funded cross-institutional project and obtained funding from Cancer Prevention Research Institute of Texas for High throughput compounds screening.
- Designed and performed biomarker discovery, proteomics, high-throughput drug screening for effectively targeting DNA damage response defective breast cancer and accessing the patient responses to immunotherapy.
- Co-developed novel biomarkers and a novel iterative resampling analysis to predict sensitivity algorithm to robustly access homologous recombination status and PARP inhibitor sensitivity.

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EDUCATION

Master in Information and Data Science, University of California, Berkeley, Berkeley, CA	2018-2020
Postdoc Fellow in Systems Biology, the University of Texas MD Anderson Cancer Center, Houston, TX	2011-2015
Ph.D. in Biochemistry and Cell Biology, Rice University, Houston, TX	
M.S. in Biochemical Sciences, National Taiwan University, Taipei, Taiwan	
B.S. in Chemistry, National Cheng Kung University, Tainan, Taiwan	1996-2000

PATENTS

International Patent Application No. PCT/US2019/020921

2019

Replication stress response biomarkers for immunotherapy response McGrail D., Lin S.Y., Pilie P, Jonasch E, <u>Lin C.C.</u>

International Patent Application No. PCT/US2014/020376

2014

Gene signature to predict homologous recombination (hr) deficient cancer **Lin C.C.**, Peng G., Lin S.Y., Mills G.B.

AWARDS

• Susan G. Komen® Scholar-in-Training Awards, American Association for Cancer Research	
• Travel Award of 5th Annual NIH National Graduate Research Festival, National Institute of Health	2011
• Dean of Wiess School of Natural Sciences Travel Grant, Rice University	2008

DATABASE SUBMISSION

Gene Expression Omnibus (GEO) database: GSE54269, GSE59227

MEMBERSHIP

- Active member, American Association for Cancer Research
- Regular member, American Society for Biochemistry and Molecular Biology

SCIECTIFIC SKILLS

Systems Biology and Data Science	Cell Biology and immunology	Cancer and Molecular Biology
R and Python programming	T cell activation and proliferation	DNA/RNA extraction
NGS and microarray data analysis	DC differentiation and maturation	qPCR
High-throughput screening (Tecan)	Macrophage phagocytosis	Molecular cloning
Gene expression analysis	B cell activation	Signaling pathways
ML/DL algorithms	Single cell sequencing	Tumorigenesis
Parallel computation with Spark	2D and 3D cell culture system	ELISA
Cloud computation and Docker	Multicolor FACS	Immunohistochemistry
SQL database and server	TAA and neoantigens	HPLC
Tableau	Antibody development	Western blot

PUBLICATIONS

McGrail DJ*, <u>Lin CC*</u>, Dai H, Mo W, Stephan C, Davies P, Lu Z, Lee JS, Lin SY (2018) Defective replication stress response is inherently linked to the cancer stem cell phenotype, *Cell Reports*, 15;23(7):2095-2106 (co-first author)

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- McGrail DJ, <u>Lin CC</u>, Garnett J, Liu Q, Mo W, Dai H, Lu Y, Yu Q, Ju Z, Yin J, Vellano CP, Hennessy B, Mills GB, Lin SY
 (2017) Improved prediction of PARP inhibitor response and identification of synergizing agents through use of a
 novel gene expression signature generation algorithm. *npj Systems Biology and Applications* 3, 8
- Wang W, Zhao J, Wen X, <u>Lin CC</u>, Li J, Huang Q, Yu Y, Lin SY, Li C (2017) MicroPET/CT Imaging of AXL Downregulation by HSP90 Inhibition in Triple-Negative Breast Cancer. *Contract Media & Molecular Imaging*, 1686525
- Mo W, Liu Q, <u>Lin CC</u>, Dai H, Peng Y, Liang Y, Peng G, Meric-Bernstam F, Mills GB, Li K, Lin SY (2016) mTOR inhibitors suppress homologous recombination repair and synergize with PARP inhibitors via regulating SUV39H1 in BRCA-proficient triple-negative breast cancer. *Clinical Cancer Research* 22, 1699
- Peng Y, Dai H, Wang E, <u>Lin CC</u>, Mo W, Peng G, Lin SY (2015). TUSC4 functions as a tumor suppressor by regulating BRCA1 stability. *Cancer Res.*, 75(2):378-86.
- Peng G*, <u>Lin CC*</u>, Mo W.*, Dai H, Park Y, Kim S, Mo Q, Peng Y, Siwko S, Hu R, Lee J, Hennessy B, Hanash S, Mills GB, Lin SY (2014) A molecular portrait of the homologous recombination DNA repair via genome-wide transcriptome profiling. *Nature Communications*, 5, 3361 (co-first author)
- Johnson C, <u>Lin CC</u>, Stern M (2012). Ras-dependent and Ras-independent effects of PI3K in Drosophila motor neurons. *Genes, Brain and Behavior*, 11, 848-858.
- <u>Lin CC</u>, Summerville J, Howlett E, Stern M (2011) The metabotropic glutamate receptor activates the lipid kinase PI3K in Drosophila motor neurons through the calcium/calmodulin-dependent protein kinase II and the nonreceptor tyrosine protein kinase DFak. *Genetics*, 188, 601
- Chen Y, Fujita T, Zhang D, Doan H, Pinkaew D, Liu Z, Wu J, Koide Y, Chiu A, <u>Lin CC</u>, Chang JY, Ruan KH, Fujise K (2011). Physical and functional antagonism between tumor suppressor protein p53 and fortilin, an anti-apoptotic protein. *J. Biol. Chem.*, 286, 32575
- Howlett E, <u>Lin CC</u>, Lavery W, Stern M (2008). A PI3 kinase-mediated negative feedback regulates Drosophila motor neuron excitability. *PloS Genetics*, 4, e1000277.
- Chang JY, <u>Lin CC</u>, Salamanca S, Pangburn MK, Wetsel RA (2008). Denaturation and unfolding of human Anapylatoxin C3a: An unusually low covalent stability of its native disulfide bonds. *Arch Biochem Biophys*, 480, 104-110.
- <u>Lin CC</u>, Chang JY (2007) Pathway of oxidative folding of bovine alpha-interferon: predominance of native disulfide-bonded folding intermediates. *Biochemistry*, 46, 3925
- Graidist P, Yazawa M, Tonganunt M, Nakatomi A, <u>Lin CC</u>, Chang JY, Phongdara A, Fujise K (2007). Fortilin binds Ca2+ and blocks Ca2+-dependent apoptosis in vivo. *Biochem J.*, 408,181-191.
- <u>Lin CC</u>, Chang JY (2006) Pathway of Oxidative Folding of Secretory Leucocyte Protease Inhibitor: An 8-disulfides protein exhibits a unique mechanism of folding. *Biochemistry*, 45, 6231
- <u>Lin CC</u>, Lu BY, Chang JY (2006). Conformational stability of Secretory Leucocyte Protease Inhibitor: a protein with no hydrophobic core and very little secondary structure. *Biochim Biophys Acta*. 1764, 1286-1291.
- Chang JY, Lu BY, <u>Lin CC</u>, Yu C. (2006). Fully oxidized scrambled isomers are essential and predominant folding intermediates of Cardiotoxin-III. *FEBS Lett.*, 580, 656.

Conference Abstracts

- <u>Lin CC</u>, Dai H, Mo W, Lin SY (2015) The Defects of Replication Stress Response Facilitate the Formation of Tumor-initiating cells. *Exploring DNA Repair Pathways as Targets for Cancer Therapy Conference*, Cancun, Mexico
- <u>Lin CC</u>, Dai H, Lin SY (2014) The replication stress response defect is associated with tumor-initiating cell formation. AACR Annual Meeting 2014. San Diego CA, USA
- Lin SY, Peng G, <u>Lin CC</u>, Mo W, Mills GB (2013) A robust gene signature predicting deficient homologous recombination DNA repair. *4th International Conference on Biomarkers & Clinical Research*. Philadelphia PA, USA
- <u>Lin CC</u>, Summerville J, Stern M (2010) CaMKII and FAK regulate neuronal homeostasis via PI3K-mediated negative feedback in Drosophila nervous system. *5th Annual NIH National Graduate Student Research Festival*. National Institute of Health, Bethesda MD, USA
- Howlett E, <u>Lin CC</u>, Lavery W, Stern M (2007) PI3K regulates neuronal excitability and axonal growth and arborization via distinct effector pathways. *The 2007 meeting on Neurobiology of Drosophila at Cold Spring Harbor Laboratory*, NY, USA.